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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/075,074

DATE: 03/01/2002 8.5
TIME: 11:45:05

Input Set : A:\EP.txt

Output Set: N:\CRF3\03012002\J075074.raw

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3 <110> APPLICANT: Brown, Arthur
4      Wible, Barbara
5      Yang, Qing
7 <120> TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on
Cell Surfaces
8      and Nucleic Acids That Encode The Same
10 <130> FILE REFERENCE: 22884/04066
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/075,074
C--> 12 <141> CURRENT FILING DATE: 2002-12-13
12 <150> PRIOR APPLICATION NUMBER: 09/062,440
13 <151> PRIOR FILING DATE: 1998-04-17
15 <150> PRIOR APPLICATION NUMBER: 09/712,495
16 <151> PRIOR FILING DATE: 2000-11-14
18 <160> NUMBER OF SEQ ID NOS: 13
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1725
24 <212> TYPE: DNA
25 <213> ORGANISM: Rattus norvegicus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(1725)
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33 Met Lys Ile Lys Glu Leu Tyr Arg Arg Phe Pro Arg Lys Thr Leu
34 1          5          10          15
36 ggg cct tcc gat ctc tct ttg ctc tct ttg ccc cct ggc acc tct cct      96
37 Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro
38          20          25          30
40 gta ggc tcc ccc agc ccc ctt gct tcc att cct ccc acc ctc ctg acc      144
41 Val Gly Ser Pro Ser Pro Leu Ala Ser Ile Pro Pro Thr Leu Leu Thr
42          35          40          45
44 cct ggc acc ttg ctg ggc cct aag cgt gag gtg gac atg cac cct cct      192
45 Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
46          50          55          60
48 ctg ccc cag cct gtg cac cct gac gtc acc atg aaa cca ctg ccc ttc      240
49 Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
50 65          70          75          80
52 tac gaa gtc tac gga gag ctc atc cgg ccg acc acc ctt gcg tcc acc      288
53 Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
54          85          90          95
56 tcc agt cag agg ttt gag gaa gcc cac ttt acc ttt gca ctc act ccc      336
57 Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro
58          100          105          110

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60 cag cag ctg cag cag att ctc aca tcc agg gag gtt ctg cca gga gcc      384
61 Gln Gln Leu Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala
62      115      120      125
64 aag tgc gat tat acc ata caa gtg cag ctc agg ttc tgt ctc tgt gag      432
65 Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu
66      130      135      140
68 acc agc tgc ccc cag gag gac tat ttc ccc cct aac ctc ttt gtc aag      480
69 Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys
70 145      150      155      160
72 gtt aat ggg aaa ctc tgc ccc ctg ccg ggt tac ctc cct cca acc aag      528
73 Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys
74      165      170      175
76 aat gga gct gag ccc aag agg cct agt cgt cca atc aac atc aca ccc      576
77 Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro
78      180      185      190
80 ctg gct cgt ctc tca gcc act gtt ccc aac acc ata gtg gtt aac tgg      624
81 Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp
82      195      200      205
84 tca tct gag ttt gga cgg aat tac tcc ttg tct gtg tac ctg gtg agg      672
85 Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg
86      210      215      220
88 cag ttg act gca ggg acc ctg cta caa aag ctc aga gcc aag ggt atc      720
89 Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile
90 225      230      235      240
92 cgg aat cca gac cat tcc cga gca ctg atc aag gag aaa ttg act gct      768
93 Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala
94      245      250      255
96 gac ccc gac agt gaa gtg gct act aca agt ctc cgg gtg tca ctc atg      816
97 Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met
98      260      265      270
100 tgc ccg ctg ggg aag atg cgc ctg act gtc cca tgc cgc gct ctc acc      864
101 Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr
102      275      280      285
104 tgt gcc cac ctg cag agt ttc gat gct gcc ctt tat cta cag atg aat      912
105 Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn
106      290      295      300
108 gag aaa aag cca aca tgg acg tgc cct gtg tgt gac aag aag gct ccc      960
109 Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro
110 305      310      315      320
112 tat gag tca ctg att att gat ggt tta ttc atg gaa att ctt aat tcc      1008
113 Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Asn Ser
114      325      330      335
116 tgt tgc gat tgt gat gag atc cag ttc atg gaa gat gga tcc tgg tgt      1056
117 Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys
118      340      345      350
120 cca atg aaa ccc aag aag gag gca tcc gag gtt tgc ccc cca cca ggg      1104
121 Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly
122      355      360      365
124 tat ggg ctg gat ggt ctc cag tat agc cca gtc cag gag gga aat cag      1152

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125 Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Glu Gly Asn Gln
126      370      375      380
128 tca gag aat aag aag agg gtt gaa gtc att gac ttg aca atc gaa agc      1200
129 Ser Glu Asn Lys Lys Arg Val Glu Val Ile Asp Leu Thr Ile Glu Ser
130 385      390      395      400
132 tca tca gat gag gaa gat ctg ccc ccc acc aag aag cac tgc cct gtt      1248
133 Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Pro Val
134      405      410      415
136 acc tcg gct gcc att cca gcc ctt cct gga agc aaa gga gcc ctg acc      1296
137 Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Ala Leu Thr
138      420      425      430
140 tct ggt cac cag ccg tct tcg gtg ctg cgg agc cct gca atg ggt aca      1344
141 Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr
142      435      440      445
144 ctg ggc agt gat ttc ctg tct agt ctc cca cta cat gag tac cca cct      1392
145 Leu Gly Ser Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro
146      450      455      460
148 gcc ttc ccg ctg ggg gct gac atc caa ggt tta gat tta ttt tct ttc      1440
149 Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe
150 465      470      475      480
152 ctt cag act gag agt cag cac tac agc cct tca gtt atc act tca cta      1488
153 Leu Gln Thr Glu Ser Gln His Tyr Ser Pro Ser Val Ile Thr Ser Leu
154      485      490      495
156 gat gag cag gac acc ctt ggc cac ttc ttc caa ttc cgg gga acc cct      1536
157 Asp Glu Gln Asp Thr Leu Gly His Phe Phe Gln Phe Arg Gly Thr Pro
158      500      505      510
160 ccc cac ttc ctg ggc cca ctg gcc ccc aca ttg ggg agc tct cac cgc      1584
161 Pro His Phe Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Arg
162      515      520      525
164 agc gcc act cca gca ccc gct cct ggc cgt gtc agc agc att gtg gct      1632
165 Ser Ala Thr Pro Ala Pro Ala Pro Gly Arg Val Ser Ser Ile Val Ala
166      530      535      540
168 cct ggg agt tcc ttg agg gaa ggg cat gga gga ccc ctg cct tcc ggt      1680
169 Pro Gly Ser Ser Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly
170 545      550      555      560
172 ccc tct ttg act ggc tgt cgg tca gac gtc att tcc ttg gac tga      1725
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174      565      570
177 <210> SEQ ID NO: 2
178 <211> LENGTH: 574
179 <212> TYPE: PRT
180 <213> ORGANISM: Rattus norvegicus
182 <400> SEQUENCE: 2
184 Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu
185 1      5      10      15
188 Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro
189      20      25      30
192 Val Gly Ser Pro Ser Pro Leu Ala Ser Ile Pro Pro Thr Leu Leu Thr
193      35      40      45

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196 Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
197      50                      55                      60
200 Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
201 65                      70                      75                      80
204 Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
205                      85                      90                      95
208 Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro
209                      100                      105                      110
212 Gln Gln Leu Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala
213                      115                      120                      125
216 Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu
217                      130                      135                      140
220 Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys
221 145                      150                      155                      160
224 Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys
225                      165                      170                      175
228 Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro
229                      180                      185                      190
232 Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp
233                      195                      200                      205
236 Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg
237                      210                      215                      220
240 Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile
241 225                      230                      235                      240
244 Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala
245                      245                      250                      255
248 Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met
249                      260                      265                      270
252 Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr
253                      275                      280                      285
256 Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn
257                      290                      295                      300
260 Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro
261 305                      310                      315                      320
264 Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Asn Ser
265                      325                      330                      335
268 Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys
269                      340                      345                      350
272 Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly
273                      355                      360                      365
276 Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Glu Gly Asn Gln
277                      370                      375                      380
280 Ser Glu Asn Lys Lys Arg Val Glu Val Ile Asp Leu Thr Ile Glu Ser
281 385                      390                      395                      400
284 Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Pro Val
285                      405                      410                      415
288 Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Ala Leu Thr
289                      420                      425                      430
292 Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr

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```

293          435          440          445
296 Leu Gly Ser Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro
297          450          455          460
300 Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe
301 465          470          475          480
304 Leu Gln Thr Glu Ser Gln His Tyr Ser Pro Ser Val Ile Thr Ser Leu
305          485          490          495
308 Asp Glu Gln Asp Thr Leu Gly His Phe Phe Gln Phe Arg Gly Thr Pro
309          500          505          510
312 Pro His Phe Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Arg
313          515          520          525
316 Ser Ala Thr Pro Ala Pro Ala Pro Gly Arg Val Ser Ser Ile Val Ala
317          530          535          540
320 Pro Gly Ser Ser Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly
321 545          550          555          560
324 Pro Ser Leu Thr Gly Cys Arg Ser Asp Val Ile Ser Leu Asp
325          565          570
328 <210> SEQ ID NO: 3
329 <211> LENGTH: 1725
330 <212> TYPE: DNA
331 <213> ORGANISM: Homo sapiens
333 <220> FEATURE:
334 <221> NAME/KEY: CDS
335 <222> LOCATION: (1)..(1725)
337 <400> SEQUENCE: 3
338 atg aag atc aaa gag ctt tac cga cga cgc ttt ccc cgg aag acc ctg      48
339 Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu
340 1          5          10          15
342 ggg ccc tct gat ctc tcc ctt ctc tct ttg ccc cct ggc acc tct cct      96
343 Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro
344          20          25          30
346 gta ggc tcc cct ggt cct cta gct ccc att ccc cca acg ctg ttg gcc      144
347 Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Leu Leu Ala
348          35          40          45
350 cct ggc acc ctg ctg ggc ccc aag cgt gag gtg gac atg cac ccc cct      192
351 Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
352          50          55          60
354 ctg ccc cag cct gtg cac cct gat gtc acc atg aaa cca ttg ccc ttc      240
355 Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
356 65          70          75          80
358 tat gaa gtc tat ggg gag ctc atc cgg ccc acc acc ctt gca tcc act      288
359 Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
360          85          90          95
362 tct agc cag cgg ttt gag gaa gcg cac ttt acc ttt gcc ctc aca ccc      336
363 Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro
364          100          105          110
366 cag caa gtg cag cag att ctt aca tcc aga gag gtt ctg cca gga gcc      384
367 Gln Gln Val Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala
368          115          120          125

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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DATE: 03/01/2002

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Input Set : A:\EP.txt

Output Set: N:\CRF3\03012002\J075074.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:864 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:888 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:891 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1048 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11